

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
2 August 2001 (02.08.2001)

PCT

(10) International Publication Number
WO 01/55174 A2

(51) International Patent Classification⁷: **C07K 1/14**

(21) International Application Number: **PCT/US00/35632**

(22) International Filing Date:
28 December 2000 (28.12.2000)

(25) Filing Language: **English**

(26) Publication Language: **English**

(30) Priority Data:
60/177,836 25 January 2000 (25.01.2000) US
60/178,368 27 January 2000 (27.01.2000) US
60/210,292 8 June 2000 (08.06.2000) US
60/210,306 8 June 2000 (08.06.2000) US

(74) Agents: **PABST, Patrea, L. et al.**; Arnall Golden & Gregory, LLP, 2800 One Atlantic Center, 1201 West Peachtree Street, Atlanta, GA 30309-3450 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(71) Applicant: **OKLAHOMA MEDICAL RESEARCH FOUNDATION** [US/US]; 825 N.E. Thirteenth Street, Oklahoma City, OK 73104 (US).

Published:

— *without international search report and to be republished upon receipt of that report*

(72) Inventor: **LIN, Xinli**; 1201 Charlton, Edmond, OK 73003 (US).

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: **UNIVERSAL PROCEDURE FOR REFOLDING RECOMBINANT PROTEINS**

WO 01/55174 A2

(57) Abstract: A universal folding method that has been demonstrated to be effective in refolding a variety of very different proteins expressed in bacteria as inclusion bodies has been developed. Representative proteins that can be dissolved and refolded in biologically active form, with the native structure, are shown in Table I. The method has two key steps to unfold and then refold the proteins expressed in the inclusion bodies. The first step is to raise the pH of the protein solution in the presence of denaturing agents to pH greater than 9, preferably 10. The protein solution may be maintained at the elevated pH for a period of up to about 24 hours, or the pH immediately decreased slowly, in increments of about 0.2 pH units/24 hours, until the solution reaches a pH of about 8.0, or both steps used. In the preferred embodiment, purified inclusion bodies are dissolved in 8 M urea, 0.1 M Tris, 1 mM glycine, 1 mM EDTA, 10 mM beta-mercaptoethanol, 10 mM dithiothreitol (DTT), 1 mM reduced glutathion (GSH), 0.1 mM oxidized glutathion (GSSG), pH 10. The absorbance at 280 nm (OD280) of the protein solution is 5.0. This solution is rapidly diluted into 20 volumes of 20 mM Tris base. The resulting solution is adjusted to pH 9.0 with 1 M HCl and is kept at 4 C for 24 hrs. The pH is adjusted to pH 8.8 and the solution is kept at 4 C for another 24 hrs. This process is repeated until the pH is adjusted to 8.0. After 24 hrs at pH8.0, the refolded proteins can be concentrated by ultrafiltration and applied to a gel filtration column for purification.

UNIVERSAL PROCEDURE FOR REFOLDING RECOMBINANT PROTEINS

Background of the Invention

5 The present invention is generally in the field of methods for manufacture of recombinant proteins, and especially in the field of refolding of recombinant proteins expressed in the inclusion bodies of procaryotic expression systems such as *E. coli*.

10 Expression of recombinant proteins with natural biological activity and structure, referred to as "proteomics", becomes increasingly important with the completion of genomic sequencing for several organisms and the near completion of human genome sequencing. One aspect of proteomics is to express large amounts of protein for structural and functional studies, as well as for commercial applications. The least expensive and most efficient
15 way to express recombinant proteins is to express the proteins in *E. coli*. Proteins are expressed either intracellularly or secreted into the periplasmic spaces. In the former case, the proteins are often deposited in inclusion bodies, especially if the protein has disulfide bonds.

20 However, one of the problems in expressing mammalian proteins in *E. coli* is that most of the expressed proteins form insoluble inclusion bodies. While this problem can be circumvented by using various mammalian or insect expression systems, growing *E. coli* is faster and less expensive compared to mammalian and insect cultures. Moreover, some proteins are toxic to the host when expressed in their native forms, thus expression as
25 insoluble inclusion bodies is the only way to obtain large quantities of recombinant proteins. Importantly, high levels of expression can be achieved for most proteins. 400 to 600 mg of inclusion bodies per liter of bacterial culture can routinely be achieved, with up to 9,700 mg/L having been reported using this method (Jeong KL; Lee SY, 1999. *Appl. Environ. Microbiol.* 65:3027-32). Inclusion bodies can be easily purified to greater
30 than 90% with a simple freeze/thaw and detergent washing procedure.

 Inclusion bodies appear as dense cytoplasmic granules when the cells are observed under a light microscope. Typically, the cells will be lysed by

mechanical disruption of the cells, followed by centrifugation for 30 min at 4700 g. Inclusion bodies will sediment at low g forces and can be separated from many other intracellular proteins. Further purification can be done by washing the pellet with the buffer used during the cell disruption, or by
5 centrifuging the resuspended pellet in 40-50% glycerol.

Many extracellular proteins of eukaryotes contain disulfide bonds. Proteins having multiple disulfide bonds may form non-native disulfide bonds during folding from the reduced species. Further folding is then blocked unless the incorrect disulfide bond is cleaved by reduction with an
10 external thiol or by attack from a protein thiol. Eukaryotic organisms that secrete disulfide containing proteins also machinery for ensuring proper disulfide bond formation. A distinct disadvantage of expression of recombinant proteins in prokaryotes as inclusion bodies is that the proteins are not obtained in their native state, and typically are not functionally active.
15 A variety of methods have been used to re-solubilize the proteins and refold them to reform active protein. Dissolution of the pelleted recombinant protein usually requires the use of denaturants such as 7 M guanidine hydrochloride or 8 M urea. The amount of aggregation may continue to increase with time if the protein is allowed to remain in the denaturant
20 (Kelley and Winkler, "Folding of Eukaryotic Proteins Produced in *Escherichia coli*" Genetic Engineering 12, 1-19 at p. 6 (1990)). Removal of the denaturant from the solubilized inclusion bodies by dialysis or desalting columns will cause the protein to precipitate under conditions where the native protein needs to be refolded. A misfolded protein solution can also
25 have a very low specific activity in biological assays.

Although there are many reports of expression and refolding of various proteins in *E. coli* as inclusion bodies, one of the misconceptions in protein refolding is that a unique refolding method has to be developed for each individual protein (see Kelley and Winkler at p. 6). Another
30 misconception is that most of the mammalian proteins cannot be refolded from inclusion bodies. (for review, see: Rudolph R., Lilie H., 1996. *FASEB J* 10:49-56; Lilie H, Schwarz E, Rudolph R. 1998. *Curr Opin Biotechnol*

9:497-501). Because published works are mostly "success" stories in refolding inclusion bodies from *E. coli*, it is impossible to get a general idea about what percentage of mammalian proteins can be purified using this procedure.

5 There are probably more refolding methods than refolded proteins reported in the literature (for review, see: Rudolph R., Lilie, H. 1996, *FASEB J* 10:49-56; Lilie, H., Schwarz, E., Rudolph, R. 1998, *Curr. Opin. Biotechnol.* 9:497-501). Different chaperones, detergents, and chaotrophs have been used to help refolding. In addition, pH, ionic strength,
10 temperature, buffer formulation, and reducing/oxidation reagents can all effect refolding. It would be prohibitive to test all these conditions for refolding large amounts of proteins, as required for studies in proteomics or structural genomics.

 A single simplified procedure to refold most of the proteins that are
15 expressed in recombinant systems, especially those which form inclusion bodies in systems such as *E. coli*, is therefore needed.

 It is therefore an object of the present invention to provide a "universal" method for refolding of proteins, especially recombinant proteins, especially recombinant proteins present in inclusion bodies in
20 bacterial hosts.

Summary of the Invention

 A universal folding method that has been demonstrated to be effective in refolding a variety of very different proteins expressed in bacteria as inclusion bodies has been developed. Representative proteins that
25 can be dissolved and refolded in biologically active form, with the native structure, are shown in Table I. The method has two key steps to unfold and then refold the proteins expressed in the inclusion bodies. The first step is to raise the pH of the protein solution in the presence of denaturing agents to pH greater than 9, preferably 10. The protein solution may be maintained at
30 the elevated pH for a period of up to about 24 hours, or the pH immediately decreased slowly, in increments of about 0.2 pH units/24 hours, until the solution reaches a pH of about 8.0, or both steps used. In the preferred

embodiment, purified inclusion bodies are dissolved in 8 M urea, 0.1 M Tris, 1 mM glycine, 1 mM EDTA, 10 mM beta-mercaptoethanol, 10 mM dithiothreitol (DTT), 1 mM reduced glutathion (GSH), 0.1 mM oxidized glutathion (GSSG), pH 10. The absorbance at 280 nm (OD280) of the protein solution is 5.0. This solution is rapidly diluted into 20 volumes of 20 mM Tris base. The resulting solution is adjusted to pH 9.0 with 1 M HCl and is kept at 4 C for 24 hr. The pH is adjusted to pH 8.8 and the solution is kept at 4 C for another 24 hrs. This process is repeated until the pH is adjusted to 8.0. After 24 hr at pH 8.0, the refolded proteins can be concentrated by ultrafiltration and applied to a gel filtration column for purification.

Detailed Description of the Invention

Expression of Recombinant Proteins

Recombinant proteins are typically expressed in a suitable host, for example, a procaryotic expression system such as *E. coli* or other type of bacteria, using a standard expression vector like a plasmid, bacteriophage or even naked DNA, and the protein expressed from the plasmid or DNA integrated the host chromosome. Suitable bacterial strains are commercially available or can be obtained from the American Type Culture Collection, Rockville, MD. (the "ATCC").

Suitable vectors can be obtained from any number of sources, including the ATCC. These need a promoter to insure that the DNA is expressed in the host, and may include other regulatory sequences. The vector may also include means for detection, such as an antibiotic resistance marker, green fluorescent protein tag, or antigen tag to facilitate in purification of the recombinant protein.

Once the DNA encoding the protein to be purified is introduced into the host, the host is cultured under appropriate conditions until sufficient amounts of recombinant protein are obtained.

Refolding/purification methods

Once the protein has been expressed in the maximum amount, it must be separated and purified from the bacterial host. The protein is isolated generally by lysing the cells, for example, by suspending in detergent, adding lysozyme, and then freezing (for example, by suspending cells in 20 ml of TN/1% TritonTM X-100, adding 10 mg lysozyme and freezing at -20°C overnight), thawing and adding DNAase to degrade all of the bacterial DNA, then washing the resulting precipitate in a buffered solution. The precipitate is then dissolved in an appropriate solution as discussed below, for refolding.

The isolated protein is then refolded. There are several critical aspects of an universal refolding method.

(i) **High pH refolding.** Most published procedures refold proteins using reducing chaotrophs (such as 8 M urea) at a physiological pH, usually pH 7.4 to 8.0. This usually produces large quantities of precipitation or aggregation, making refolding either impossible or with a very low yield. It has been found that some proteins cannot be refolded at physiological pH, but can be refolded when initial refolding pH is high (at least pH 9.0, although higher pH, such as pH 10, may be desirable). This strategy was initially inspired by the fact that pepsinogen can be reversibly denatured/renatured between pH 8.0 and 9.0. It is postulated that at high pH (such as pH 9.0), proteins can obtain some secondary structures, allowing it to be refolded more efficiently when acidity of the refolding solution is lowered to the biological pH. Later it was found that even for the proteins that could be refolded at a physiological pH, high pH refolding resulted in a better yield. In addition, high pH refolding is an excellent method for preventing initial large scale precipitation.

(ii) **Non-denaturing chaotroph concentration.** It has been shown in several labs that non-denaturing concentrations of chaotrophic reagents, such as 0.5 to 1.0 M of urea, guanidine hydrochloride, and L-arginine, can be used to assist refolding and stabilize refolded proteins (Rudolph et al. 1996, *FASEB J* 10:49-56). The preferred concentration of chaotrophic reagents is 0.4 M, although the concentration may range from 0

to 4 M. A moderate concentration of urea in the refolding/purification procedures has not been found to have a denaturing effect on proteins.

(iii) **Reducing/oxidation reagents.** Inclusion bodies for mammalian proteins containing disulfide bonds need to be dissolved in the presence of reducing reagents. Representative reducing agents include beta-mercaptoethanol, in a range of from 0.1 mM to 100 mM, preferably 10 mM; DTT, in a range of from 0.1 mM to 10 mM, preferably 10 mM; reduced glutathion (GSH), in a range from 0.1 mM to 10 mM, preferably 1 mM; and oxidized glutathion (GSSG), in a range from 0.1 mM to 10 mM, preferably 1 mM. Beta-mercaptoethanol is a preferred reducing reagent. In addition, dithiothreitol and/or reduced/oxidized glutathion (GSH, GSSG) can also be included to facilitate "oxido-shuffling" of wrongly folded, intermediate disulfide bonds.

(iv) **pH control** It is important that the protein solution remain at an elevated condition long enough to refold the protein. This is preferably achieved by decreasing the pH slowly, in 0.2 pH unit increments per 24 hours. In this method, the protein solution is adjusted to a high pH, preferably at least 9.0 or higher, to 10 or less preferably 11. The protein is preferably maintained at each pH for at least 24 hours, although comparable effects can be achieved with shorter periods of time, for example, for a period of three, six, nine, twelve, eighteen or twenty hours, most preferably at least twelve hours. The pH can be adjusted by addition of an acid or by dialysis or dilution into a lower pH. Addition of the acid is preferred.

The four conditions discussed above are considered the most essential aspects of the basic protocol for the "universal" refolding procedure.

Table I. Expression, refolding, and purification of different proteins from *E. coli*

Name	From	Organism	Refold	Purification	Ref.
Pepsinogen	Full-length	Porcine	Yes	Yes	Lin, et al, 1989
Pepsinogen	N and C Domain	Porcine	Yes	Yes	Lin, et al, 1992
Rhizopus-Pepsinogen	full-length	Fungus	Yes	Yes	Lin, et al, 1993
Thermopsin	full-length	Archae	No	No	Chen, et al, 1991
Thermopsin	fusion	Archae	Yes	Partial	Lin, et al, 1992
Cathepsin D	full-length	human	No	No	None
Pregnancy Specific Ant	full-length	Bovine	No	No	low yield
HIV protease	full-length	Ovine	No	No	None
SAP	full-length	HIV	Yes	Yes	Lin, et al, 1995
Streptokinase	full-length	Yeast	Yes	Yes	Ermolief, et al, 97
Plasminogen	full-length	bacteria	Yes	Yes	Lin, et al, 1993
Cadosin A	cat-domain	human	Yes	Yes	Koelsch, et al, 98
	full-length	plant	Yes	Yes	Wang, et al, 1998
					Wang, et al, 2000
					Faro, et al, 1999

Napsin 1	full-length	human	No	No	Koelsch, et al, 00
Memapsin 2	full-length	human	Yes	Yes	Lin, et al, 2000
Memapsin 1	full-length	human	Yes	Yes	
PreS	partial	HBV	Yes	Yes	
unc-76	full-length	C. elegans	Yes	Yes	
odc-1	full-length	C. elegans	Yes	Yes	
ceh-10	full-length	C. elegans	Yes	Yes	
ppp-1	full-length	C. elegans	No	No	

∞

References for Table 1:

- Lin, X, Wong, R.N.S., and Tang, J. (1989) "Synthesis, purification, and active site mutagenesis of recombinant porcine pepsinogen". *J. Biol. Chem.* 264:4482-4489.
- Lin, X.L., Lin, Y.-Z., Koelsch, G., Gustchina, A., Wlodawer, A., and Tang, J. (1992) "Enzymic activities of two-chain pepsinogen, two-chain pepsin, and the amino-terminal lobe of pepsinogen". *J. Biol. Chem.* 267:17257-17263.
- Lin, X., Loy, J.A., Sussman, F., and Tang, J. (1993) "Conformational instability of the N- and C-terminal lobes of porcine pepsin in neutral and alkaline solutions". *Pro. Sci.* 2:1383-1390.
- Chen, Z., Koelsch, G., Han, H.-P., Wang, X.-J., Lin, X., Hartsuck, J.A., and Tang, J. (1991) "Recombinant rhizopuspepsinogen", *J. Biol. Chem.* 266:11718-11725.
- Lin, Y.-Z., Fusek, M., Lin, X.L., Hartsuck, J.A., Kezdy, F.J., and Tang, J. (1992) "pH Dependence of kinetic parameters of pepsin, rhizopuspepsin, and their active-site hydrogen bond mutants". *J. Biol. Chem.* 267:18413-18418.
- Lin, X.L., Liu, M.T., and Tang, J. (1992) "Heterologous expression of thermopsis, a heat stable acid proteinase". *Enzyme Microb. Technol.* 14:696-701.

- Lin, Y.-Z., Lin, X., Hong, L., Foundling, S., Heinrichson, R.L., Thaisrivongs, S., Leelamanit, W., Raterman, D., Shah, M., Dunn, B.M., and Tang, J. (1995) "Effect of point mutations on the kinetics and the inhibition of human immunodeficiency virus type 1 protease: relationship to drug resistance". *Biochemistry* 34:1143-1152.
- Ermoloeff, J., Lin, X., and Tang, J. (1997) Kinetic properties of saquinavir-resistant mutants of human immunodeficiency virus type 1 protease and their implications in drug resistance *in vivo*. *Biochemistry* 36:12364-12370.
- Lin, X., Tang, J., Koelsch, G., Monod, M., and Foundling, S. (1993) "Recombinant candidropsin, an extracellular aspartic protease from yeast *Candida tropicalis*". *J. Biol. Chem.* 268_20143-20147.
- Koelsch, G., Tang, J., Monod, M., Foundling, S.I., Lin, X. (1998) "Primary substrate specificities of secreted aspartic proteases of *Candida albicans*". *Adv. Exp. Med. Biol.* 436:335-338.
- Wang, X., Lin, X., Lowy, J.A., Tang, J., Zhang, X.C. (1998) "Crystal structure of the catalytic domain of human plasmin complexed with streptokinase", *Science*. 281:1662-1665.
- Wang, X., Terzyan, S., Tang, J., Loy, J., Lin, X., and Zhang, X. (2000) "Human plasminogen catalytic domain undergoes a novel conformational change upon activation" *J. Mol. Biol.* (in press).
- Faro, C., Ramalho-Santos, M., Vieira, M., Mendes, A., Simoes, I., Andrade, R., Verissimo, P., Lin, X., Tang, J., Pires, E. (1999) "Cloning and Characterization of cDNA Encoding Cardosin A, an RGD-containing Plant Aspartic Proteinase," *J. Biol. Chem.* 274(40):28724-28729.
- Lin, X., Koelsch, G., Wu, S., Downs, D., Dashti, A., and Tang, J. (2000) "Human aspartic protease memapsin 2 cleaves the -secretase site of -amyloid precursor protein. *Proc. Natl. Aca. Sci.* 97(4):1456-1460.
- Ghosh, A.K., Shin, D., Downs, D., Koelsch, G., Lin, X., Ermoloeff, J., Tang, J. (2000) "Design of potent inhibitors from human brain memapsin 2 (-secretase)" *J. Amer. Chem. Soc.*, 122:3522-3523.

The present invention will be further understood by reference to the following non-limiting examples.

Example 1: Preferred Method for Refolding Recombinant Proteins

A. Reagents:

- 5 ZB media: 10 g N-Z-Amine A, 5 g NaCl/L
 LB media: 10 g Tryptone, 5 g Yeast extract, 10 g NaCl/L, pH 7.5
 8 M urea: 8 M urea, 0.1 M TRISTM, 1 mM glycine, 1 mM EDTA, pH 10
 TN buffer: 0.05 mM TRISTM, 0.15 M NaCl, pH 7.5

B. Expression of the Recombinant Protein:

- 10 1. Expression plasmids should be transfected into an appropriate host, such as the BL21(DE3) strain of *E. coli* and plated on ZB/Ampicillin plates, which selects for the desired recombinant organisms. A single colony from each construct is inoculated into 100 ml of ZB/ampicillin media and grown 16 h at 37°C.
- 15 2. Inoculate 20 ml of the overnight culture into 1 L of LB/ampicillin, and shake at 37°C till OD₆₀₀ reaches 0.4-0.6. Add IPTG to 0.5 mM, then shake for 3 h.
3. Centrifuge and resuspend cells in 20 ml of TN/1% TritonTM X-100. Add 10 mg lysozyme and freeze at -20°C overnight.
- 20 4. Thaw the frozen cells, add 20 µl 1 M MgSO₄ 100 µg DNAase, and stir until the bacterial DNA is completely dissolved.
5. Add 250 ml of TN/1% Triton and stir for 2-4h. Centrifuge and repeat the Triton wash one more time.
6. Dissolve the pellet in 10 ml of 8 M urea solution, add beta-
25 Mercaptoethanol to 100 mM. This solution can be ultracentrifuged, and is then ready for refolding.

C. Refolding and purification:

- The OD₂₈₀ of the solution containing the inclusion bodies is adjusted to 5.0 with the 8 M urea solution. The final solution contains the following
30 reducing reagents:
 10 mM beta-Mercaptoethanol

10 mM DTT (Dithiothreitol)

1 mM reduced glutathion (GSH)

0.1 mM oxidized glutathion (GSSG)

The final pH of the solution is 10.0.

5 1. The above solution is rapidly diluted into 20 volumes of 20 mM TRISTM base, the pH is adjusted to 9.0, and then slowly adjusted to 8.0 with 1 M HCl, by adjusting pH to 8.8 for twenty four hours, then 8.6 for twenty four hours, etc., until the pH is 8.0. Alternatively, the proteins can be refolded using dialysis. The OD₂₈₀ of the 8 M urea solution is adjusted to 0.5, and dialyzed
10 against 20 volumes of TRISTM base. The pH of the solution is again slowly adjusted to 8.0.

2. The refolded material is then concentrated by ultrafiltration, and separated by gel filtration, for example, on a SEPHACRYLTM S-300 column equilibrated with 20 mM TRISTM, HCl, 0.4 M urea, pH 8.0.

15 3. The S-300 fractions can be checked by running a non-reduced SDS-PAGE. The wrongly refolded protein runs at a very high molecular weight, while folded proteins run at a normal molecular weight.

4. The refolded peak from the S-300 column can be further purified with a FPLC Resource-QTM or Resource-STM column, which is equilibrated with
20 20 mM TRISTM-HCl (HEPES buffer for Resource-STM), 0.4 M urea, pH 8.0.

The enzyme is eluted from the column with a linear gradient of NaCl.

Table I lists all of the proteins which have been refolded directly or as inclusion bodies.

Example 2. Expression and Refolding of memapsin 2.

25 Pro-memapsin 2 was PCR amplified and cloned into the *Bam*HI site of a pET11a vector. The resulting vector expresses pro-memapsin 2 having a sequence from Ala-8p to Ala-326. Two expression vectors, pET11-memapsin 2-T1 (hereafter T1) and pET11-memapsin 2-T2 (hereafter T2), were constructed. In both vectors, the N-terminal 15 residues of the expressed recombinant
30 proteins are derived from the expression vector. Pro-memapsin 2 residues start at residue Ala-16. The two recombinant pro-memapsin 2s have different C-

terminal lengths. Clone T1 ends at Thr- 454 and clone T2 ends at Ala-419. The T1 construct contains a C-terminal extension from the T2 construct but does not express any of the predicted transmembrane domain.

The T1 and T2 expression vectors were separately transfected into *E. coli* strain BL21(DE3). The procedures for the culture of transfected bacteria, induction for synthesis of recombinant proteins and the recovery and washing of inclusion bodies containing recombinant proteins are essentially as described by Lin et al., 1994 Methods in Enzymology 214, 195-224. Basically, the inclusion bodies are washed with 1% (v/v) Triton X-100 and 0.15 M NaCl in 0.1 M TrisTM HCl, pH 7.4, the insoluble protein is dissolved in a solution containing 8 M urea, 0.05 M cyclohexylaminopropanesulfonic acid, 10 mM 2-mercaptoethanol, 10 mM DTT (Dithiothreitol), 1 mM reduced glutathion (GSH), 0.1 mM oxidized glutathion (GSSG), 1 mM glycine, and 1 mM ethylenediaminetetraacetic acid (EDTA), pH 10.5, to a protein concentration of about 5 mg/ml. This solution is added dropwise to 20 vol of rapidly stirred 20 mM Tris base. The pH of the diluted solution is readjusted to 9.0 with 1 M HCl and kept at 4 C for 24 hr. The pH is then adjusted to 8.8 with 1 M HCl, and kept at 4 C for 24 hr again. The process is repeated until the pH is adjusted to 8.0.

Three different refolding methods have produced satisfactory results.

(i) *The rapid dilution method.*

Pro-memapsin 2 in 8 M urea/10 mM DTT (Dithiothreitol), 1 mM reduced glutathion (GSH), 0.1 mM oxidized glutathion (GSSG), with OD_{280nm} = 5 was rapidly diluted into 20 volumes of 20 mM-Tris base. The solution was slowly adjusted into pH 8 with 1 M HCl. The refolding solution was then kept at 4° C for 24 to 48 hours before proceeding with purification.

(ii) *The reverse dialysis method*

An equal volume of 20 mM TRISTM, 0.5 mM oxidized/1.25 mM reduced glutathione, pH 9.0 is added to rapidly stirred pro-memapsin 2 in 8 M urea/10 mM beta-mercaptoethanol with OD_{280 nm} = 5. The process is repeated three more times with 1 hour intervals. The resulting solution is then dialyzed against

sufficient volume of 20 mM TRIS™ base so that the final urea concentration is 0.4 M. The pH of the solution is then slowly adjusted to 8.0 with 1 M HCl.

iii. *The preferred method for refolding.*

Inclusion bodies are dissolved in 8 M urea, 0.1 M TRIS™, 1 mM
5 Glycine, 1 mM EDTA, 100 mM beta-mercaptoethanol, pH 10.0. The OD₂₈₀ of the inclusion bodies are adjusted to 5.0 with the 8 M urea solution without beta-mercaptoethanol. The final solution contains the following reducing reagents: 10 mM beta-mercaptoethanol, 10 mM DTT (Dithiothreitol), 1 mM reduced glutathion, and 0.1 M oxidized glutathion. The final pH of the solution is 10.0.
10 The above solution is rapidly diluted into 20 volumes of 20 mM TRIS™ base, the pH is adjusted to 9.0, and the resulting solution is kept at 4 °C for 16 hr. The solution is equilibrated to room temperature in 6 hr, and the pH is adjusted to 8.5. The solution is returned to 4 °C again for 18 hr.

The solution is again equilibrated to room temperature in 6 hr, and the
15 pH is adjusted to 8.0. The solution is returned to 4 °C again for 4 to 7 days.

Purification of recombinant pro-memapsin 2-T1

The refolded material is concentrated by ultrafiltration, and separated on a SEPHACRYL™ S-300 column equilibrated with 20 mM TRIS™ HCl, 0.4 M urea, pH 8.0. The refolded peak (second peak) from the S-300 column can be
20 further purified with a FPLC RESOURCE-Q™ column, which is equilibrated with 20 mM TRIS™-HCl, 0.4 M urea, pH 8.0. The enzyme is eluted from the column with a linear gradient of NaCl. The refolded peak from S-300 can also be activated before further purification. For activation, the fractions are mixed with equal volume 0.2 M Sodium Acetate, 70% glycerol, pH 4.0. The mixture is
25 incubated at 22 °C for 18 hr, and then dialyzed twice against 20 volumes of 20 mM Bis-TRIS™, 0.4 M urea, pH 6.0. The dialyzed materials are then further purified on a FPLC RESOURCE-Q™ column equilibrated with 20 Bis-TRIS™, 0.4 M urea, pH 6.0. The enzyme is eluted with a linear gradient of NaCl.

Modifications and variation of these methods are intended to come
30 within the scope of the appended claims.

I claim:

1. A method for refolding of recombinant proteins comprising maintaining the protein at a pH of 9.0 or greater, in the presence of one or more chaotropic and reducing agents, and decreasing the pH of the solution gradually over a period of at least about 24 hrs to pH 8.0 to induce renaturation of at least a portion of the protein so that it qualitatively exhibits a biological activity and structure characteristic of the protein.
2. The method of claim 1 wherein pH is decreased in increments equivalent to 0.2 pH units per 24 hours.
3. The method of claim 1 wherein the protein is maintained at a pH of greater than 9.0 for a period of at least 24 hours.
4. The method of claim 1 wherein the pH is decreased by addition of acid.
5. The method of claim 1 wherein the pH is decreased by dilution or dialysis into a solution of a lower pH.
6. The method of claim 1 wherein the chaotropic and denaturing reagents are selected from the group consisting of between .5 and 1.0 M urea, 0.1 mM to 100 mM beta-mercaptoethanol, 0.1 mM to 100 mM DTT, 0.1 mM to 10 mM reduced glutathion, and 0.1 mM to 10 mM oxidized glutathion.
7. The method of claim 1 wherein the protein is first extracted from bacterial inclusion bodies.
8. The method of claim 4 wherein the bacteria is *E. coli*.
9. The method of claim 7 wherein the inclusion bodies are dissolved at a final pH of between greater than 9 and 10.
10. The method of claim 1, wherein the protein is dissolved at a pH above about 10.0.
11. The method of claim 1, wherein the protein is dissolved at a pH above about 11.0.
12. The method of claim 1, wherein the protein is dissolved at a pH above about 12.0.

13. The method of claim 1 wherein the pH is decreased over a period of at least about 36 hours.
14. The method of claim 1, wherein the pH of the solution is reduced more quickly at the higher pH and more gradually nearer the physiological pH range of the protein.
15. The method of claim 1 comprising the additional step of separating protein species which exhibits biological activity from inactive, or wrongly folded, protein species.